

SEQUENCE LISTING

<110> Young, John A.T.
Bradley, Kenneth A.
Collier, Robert J.
Mogridge, Jeremy S.

<120> Anthrax Toxin Receptor

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<151> 2000-12-05

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<170> PatentIn Ver. 2.1

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Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly
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cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259
Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
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gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307
Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
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Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
70 75 80

tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc 1075
 Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala
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atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg 1123
 Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp
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 Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro
 345 350 355

ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag 1217
 Pro Pro Ala Glu Ser Glu Glu Asn Lys Ile Lys
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tacaatgctc tgaaaatcat agtctcaatc tagacagtct tttcctctag ttcctgtat 1337

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 35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
 50 55 60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
 130 135 140

Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu	Leu	His	Glu	Asp	Leu	Phe	Phe	Tyr	145	150	155	160
Ser	Glu	Arg	Glu	Ala	Asn	Arg	Ser	Arg	Asp	Leu	Gly	Ala	Ile	Val	Tyr	165	170	175	
Cys	Val	Gly	Val	Lys	Asp	Phe	Asn	Glu	Thr	Gln	Leu	Ala	Arg	Ile	Ala	180	185	190	
Asp	Ser	Lys	Asp	His	Val	Phe	Pro	Val	Asn	Asp	Gly	Phe	Gln	Ala	Leu	195	200	205	
Gln	Gly	Ile	Ile	His	Ser	Ile	Leu	Lys	Lys	Ser	Cys	Ile	Glu	Ile	Leu	210	215	220	
Ala	Ala	Glu	Pro	Ser	Thr	Ile	Cys	Ala	Gly	Glu	Ser	Phe	Gln	Val	Val	225	230	235	240
Val	Arg	Gly	Asn	Gly	Phe	Arg	His	Ala	Arg	Asn	Val	Asp	Arg	Val	Leu	245	250	255	
Cys	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	Thr	Leu	Asn	Glu	Lys	Pro	Phe	260	265	270	
Ser	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	Pro	Ala	Pro	Ile	Leu	Lys	Glu	275	280	285	
Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser	Met	Asn	Asp	Gly	Leu	Ser	290	295	300	
Phe	Ile	Ser	Ser	Ser	Val	Ile	Ile	Thr	Thr	Thr	His	Cys	Ser	Asp	Gly	305	310	315	320
Ser	Ile	Leu	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Leu	Ala	Leu	325	330	335	
Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	Cys	Cys	Thr	Val	Ile	Ile	Lys	340	345	350	
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<223> Description of Artificial Sequence: von Willebrand
factor A domain consensus sequence

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Asn Arg Phe Glu Leu Ala Lys Glu Phe Val Leu Lys Leu Val Glu Gln
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 Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser
 35 40 45
 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
 50 55 60
 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
 65 70 75 80
 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
 85 90 95
 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
 100 105 110
 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
 115 120 125
 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
 130 135 140
 Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
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 Asp Leu Leu Leu
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 <213> Homo sapiens

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 35 40 45
 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
 50 55 60
 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp
 65 70 75 80

Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
 85 90 95
 Ser Ala Ser Gly Gly Arg Arg Ser Ala Ala Thr Lys Val Met Val Val
 100 105 110
 Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
 115 120 125
 Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
 130 135 140
 Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
 145 150 155 160
 Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
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 ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gcc ctc ggc 173
 Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
 1 5 10
 atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
 Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
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 ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
 Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
 30 35 40
 ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac 317
 Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
 45 50 55

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Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile	
60 65 70	
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca	413
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr	
75 80 85 90	
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta	461
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu	
95 100 105	
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa	509
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu	
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gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg	557
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly	
125 130 135	
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat	605
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His	
140 145 150	
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat	653
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp	
155 160 165 170	
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca	701
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr	
175 180 185	
cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat	749
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn	
190 195 200	
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Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys	
205 210 215	
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga	845
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly	
220 225 230	
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Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg	
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Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr	
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Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu	
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Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys	
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Gln Pro Ala Lys Tyr Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro	
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cct cct gcc ccc atc tac act ccc cca cct cct gcg ccc cac tgc cct 1709
 Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Pro Ala Pro His Cys Pro
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ccc ccg ccc ccc agc gcc cct acc cct ccc atc ccg tcc cca cct tcc 1757
 Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser
 525 530 535

acc ctt ccc cct cct ccc cag gct cca cct ccc aac agg gca cct cct 1805
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 35 40 45
 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
 50 55 60
 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
 65 70 75 80
 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
 85 90 95
 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
 100 105 110
 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
 115 120 125

Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
 130 135 140
 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
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 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
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 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
 180 185 190
 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
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 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
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 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
 225 230 235 240
 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
 245 250 255
 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
 260 265 270
 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
 275 280 285
 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
 290 295 300
 Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
 305 310 315 320
 Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
 325 330 335
 Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
 340 345 350
 Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Glu Asp Asp Asp
 355 360 365
 Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly
 370 375 380
 Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
 385 390 395 400
 Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
 405 410 415
 Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
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Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
435 440 445

Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
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Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465 470 475 480

Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
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Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
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Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
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<222> (113)..(1111)

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Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu
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Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp
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Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
35 40 45 50

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Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val	
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Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe	
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Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp	
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Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro	
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Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln	
115 120 125 130	
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Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile	
135 140 145	
gct ttg act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag	598
Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu	
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agg gag gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt	646
Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val	
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ggt gtg aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt	694
Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser	
180 185 190	
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Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly	
195 200 205 210	
atc atc cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct	790
Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala	
215 220 225	
gaa cca tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga	838
Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg	
230 235 240	
gga aac ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc	886
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser	
245 250 255	
ttc aag atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg	934
Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val	
260 265 270	

gaa gat act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc 982
 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
 275 280 285 290

 atg aaa gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc 1030
 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
 295 300 305

 tcc agt tct gtc atc atc acc acc aca cac tgt agc ctc cac aaa att 1078
 Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Leu His Lys Ile
 310 315 320

 gca tca ggc ccc aca aca gct gct tgc atg gaa tagcagagaa taccgcctgc 1131
 Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
 325 330

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<212> PRT

<213> Homo sapiens

<400> 8

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Ser	Leu	Ala	Thr	Leu	Val	Leu	Ile	Cys	Ala	Gly	Gln	Gly	Gly	Arg	Arg	20	25	30	
Glu	Asp	Gly	Gly	Pro	Ala	Cys	Tyr	Gly	Gly	Phe	Asp	Leu	Tyr	Phe	Ile	35	40	45	
Leu	Asp	Lys	Ser	Gly	Ser	Val	Leu	His	His	Trp	Asn	Glu	Ile	Tyr	Tyr	50	55	60	
Phe	Val	Glu	Gln	Leu	Ala	His	Lys	Phe	Ile	Ser	Pro	Gln	Leu	Arg	Met	65	70	75	80
Ser	Phe	Ile	Val	Phe	Ser	Thr	Arg	Gly	Thr	Thr	Leu	Met	Lys	Leu	Thr	85	90	95	
Glu	Asp	Arg	Glu	Gln	Ile	Arg	Gln	Gly	Leu	Glu	Glu	Leu	Gln	Lys	Val	100	105	110	
Leu	Pro	Gly	Gly	Asp	Thr	Tyr	Met	His	Glu	Gly	Phe	Glu	Arg	Ala	Ser	115	120	125	
Glu	Gln	Ile	Tyr	Tyr	Glu	Asn	Arg	Gln	Gly	Tyr	Arg	Thr	Ala	Ser	Val	130	135	140	
Ile	Ile	Ala	Leu	Thr	Asp	Gly	Glu	Leu	His	Glu	Asp	Leu	Phe	Phe	Tyr	145	150	155	160
Ser	Glu	Arg	Glu	Ala	Asn	Arg	Ser	Arg	Asp	Leu	Gly	Ala	Ile	Val	Tyr	165	170	175	
Cys	Val	Gly	Val	Lys	Asp	Phe	Asn	Glu	Thr	Gln	Leu	Ala	Arg	Ile	Ala	180	185	190	
Asp	Ser	Lys	Asp	His	Val	Phe	Pro	Val	Asn	Asp	Gly	Phe	Gln	Ala	Leu	195	200	205	
Gln	Gly	Ile	Ile	His	Ser	Ile	Leu	Lys	Lys	Ser	Cys	Ile	Glu	Ile	Leu	210	215	220	
Ala	Ala	Glu	Pro	Ser	Thr	Ile	Cys	Ala	Gly	Glu	Ser	Phe	Gln	Val	Val	225	230	235	240
Val	Arg	Gly	Asn	Gly	Phe	Arg	His	Ala	Arg	Asn	Val	Asp	Arg	Val	Leu	245	250	255	
Cys	Ser	Phe	Lys	Ile	Asn	Asp	Ser	Val	Thr	Leu	Asn	Glu	Lys	Pro	Phe	260	265	270	
Ser	Val	Glu	Asp	Thr	Tyr	Leu	Leu	Cys	Pro	Ala	Pro	Ile	Leu	Lys	Glu	275	280	285	
Val	Gly	Met	Lys	Ala	Ala	Leu	Gln	Val	Ser	Met	Asn	Asp	Gly	Leu	Ser	290	295	300	

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His
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Lys Ile Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu
325 330

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catcagccca cagttgaga atg tcc ttt att gtt ttc tcc acc cga gga aca 412
Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
1 5 10
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 460
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
15 20 25
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 508
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu
30 35 40
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg 556
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly
45 50 55
tac agg aca gct agc gtc atc att gct ttg act gat gga gaa ctc cat 604
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His
60 65 70 75
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat 652
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp
80 85 90
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca 700
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr
95 100 105

cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat 748
 Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn
 110 115 120

gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag 796
 Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys
 125 130 135

tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga 844
 Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly
 140 145 150 155

gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc 892
 Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg
 160 165 170

aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca 940
 Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr
 175 180 185

ctc agt aag tcc ttg cag agt cca tgg gtt tct tcg aca agt ggc ttc 988
 Leu Ser Lys Ser Leu Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe
 190 195 200

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 Lys Glu Gly Asn Ser His Pro Cys Leu Pro Ala Arg Pro His Thr
 205 210 215

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 Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys
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